            inputting a plurality of probe intensities, each of
said plurality of probe intensities being associated with a
nucleic acid probe and substantially proportional to said
associated nucleic acid probe hybridizing with said sample
sequence;

            said computer system comparing at least one of said
plurality of probe intensities with said statistics; and

            calling said unknown base according to results of said
comparing step.

            58. The method of claim 57, further comprising the
step of calculating said statistics.

            59. The method of claim 57, wherein said statistics
include a mean and standard deviation.--

                              REMARKS

            Claims 1, 3-20 and 45-59 are pending in the subject
application. Applicants canceled claims 2 and 21-44 without
prejudice and reserve all right to pursue these or other claims
in another application.

                              Respectfully submitted,

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